OFFICE OF THE DIRECTOR OF NATIONAL INTELLIGENCE

NATIONAL INTELLIGENCE COUNCIL



Updated Assessment on

COVID-19 ORIGINS

Updated Assessment on COVID-19 Origins

Key Takeaways

Scope Note: This assessment responds to the President's request that the Intelligence Community (IC) update its previous judgments on the origins of COVID-19. It also identifies areas for possible additional research. Annexes include a lexicon, additional details on methodology, and comments from outside experts. This assessment is based on information through August 2021.

The IC assesses that SARS-CoV-2, the virus that causes COVID-19, probably emerged and infected humans through an initial small-scale exposure that occurred no later than November 2019 with the first known cluster of COVID-19 cases arising in Wuhan, China in December 2019. In addition, the IC was able to reach broad agreement on several other key issues. We judge the virus was not developed as a biological weapon. Most agencies also assess with low confidence that SARS-CoV-2 probably was not genetically engineered; however, two agencies believe there was not sufficient evidence to make an assessment either way. Finally, the IC assesses China's officials did not have foreknowledge of the virus before the initial outbreak of COVID-19 emerged.

After examining all available intelligence reporting and other information, though, the IC remains divided on the most likely origin of COVID-19. All agencies assess that two hypotheses are plausible: natural exposure to an infected animal and a laboratory-associated incident.

- Four IC elements and the National Intelligence Council assess with low confidence that the initial SARS-CoV-2 infection was most likely caused by natural exposure to an animal infected with it or a close progenitor virus—a virus that probably would be more than 99 percent similar to SARS-CoV-2. These analysts give weight to China's officials' lack of foreknowledge, the numerous vectors for natural exposure, and other factors.

- One IC element assesses with moderate confidence that the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling by the Wuhan Institute of Virology. These analysts give weight to the inherently risky nature of work on coronaviruses.

- Analysts at three IC elements remain unable to coalesce around either explanation without additional information, with some analysts favoring natural origin, others a laboratory origin, and some seeing the hypotheses as equally likely.

- Variations in analytic views largely stem from differences in how agencies weigh intelligence reporting and scientific publications and intelligence and scientific gaps.

The IC judges they will be unable to provide a more definitive explanation for the origin of COVID-19 unless new information allows them to determine the specific pathway for initial natural contact with an animal or to determine that a laboratory in Wuhan was handling SARS-CoV-2 or a close progenitor virus before COVID-19 emerged.

- The IC—and the global scientific community—lacks clinical samples or a complete understanding of epidemiological data from the earliest COVID-19 cases. If we obtain information on the earliest cases that identified a location of interest or occupational exposure, it may alter our evaluation of hypotheses.

China's cooperation most likely would be needed to reach a conclusive assessment of the origins of COVID-19. Beijing, however, continues to hinder the global investigation, resist sharing information, and blame other countries, including the United States. These actions reflect, in part, China's government's own uncertainty about where an investigation could lead as well as its frustration the international community is using the issue to exert political pressure on China.

AREAS OF BROAD AGREEMENT

- First known cluster of COVID-19 cases emerged in Wuhan, China in December 2019
- Virus not developed as a biological weapon
- Virus not genetically engineered
- China's officials unaware of virus before pandemic emerged

TWO PLAUSIBLE HYPOTHESES ON INITIAL HUMAN EXPOSURE

- Natural transmission from animal to human
- Laboratory-associated incident
- Evidence not strongly diagnostic of either hypothesis

CHINA'S COOPERATION KEY TO UNDERSTANDING ORIGINS

- Beijing's lack of cooperation on origins not diagnostic of either hypothesis
- Numerous information gaps, particularly related to technical data

Introduction

The IC has prepared several assessments examining the origins of COVID-19. Analysts have focused on whether SARS-CoV-2, the causative virus of COVID-19, was genetically engineered—particularly as a biological weapon—was transmitted to humans naturally or transmitted due to a laboratory-associated incident, perhaps during sampling or experimentation. China's reaction to and handling of the pandemic have given analysts insights into these issues, but Beijing's actions have also impeded the global scientific community and our ability to confidently determine how the virus first infected humans.

SARS-CoV-2 Probably Not a Biological Weapon

The IC assesses China did not develop SARS-CoV-2 as a biological weapon.

- We remain skeptical of allegations that SARS-CoV-2 was a biological weapon because they are supported by scientifically invalid claims, their proponents do not have direct access to the Wuhan Institute of Virology (WIV), or their proponents are suspected of spreading disinformation. [*See appendix B.*]

Most Analysts Assess SARS-CoV-2 Not Genetically Engineered

Most IC analysts assess with low confidence that SARS-CoV-2 was not genetically engineered. Their assessment is based on technical analysis of SARS-CoV-2 and the IC's growing understanding of traits and the potential for recombination in other coronaviruses. Two agencies believe there is not sufficient evidence to make an assessment either way.

- As of August 2021, we still have not observed genetic signatures in SARS-CoV-2 that would be diagnostic of genetic engineering, according to the IC's understanding of the virus. Similarly, we have not identified any existing coronavirus strains that could have plausibly served as a backbone if SARS-CoV-2 had been genetically engineered.

- Our growing understanding of the similarities of SARS-CoV-2 to other coronaviruses in nature and the ability of betacoronaviruses—the genus to which SARS-CoV-2 belongs—to naturally recombine suggests SARS-CoV-2 was not genetically engineered. For instance, academic literature has noted that in some instances betacoronaviruses have recombined with other viruses in nature and that furin cleavage sites (FCS)—a region in the spike protein that enhances infection—have been identified in naturally occurring coronaviruses in the same genetic location as the FCS in SARS-CoV-2. This suggests that SARS-CoV-2 or a progenitor virus could have acquired its FCS through natural recombination with another virus.

IC analysts do not have higher confidence that SARS-CoV-2 was not genetically engineered because some genetic engineering techniques can make modifications difficult to identify and we have gaps in our knowledge of naturally occurring coronaviruses.

- Some genetic engineering techniques may make genetically modified viruses indistinguishable from natural viruses, according to academic journal articles. For instance, a 2017 dissertation by a WIV student showed that reverse genetic cloning techniques—which are standard techniques used in advanced molecular laboratories—left no trace of genetic modification of SARS-like coronaviruses.

- It will be difficult to increase our confidence that the distinguishing features in SARS-CoV-2 emerged naturally without a better understanding of the diversity of coronaviruses in nature and how often recombination occurs during co-infection of multiple coronaviruses within a particular host. For example, academic literature has indicated that a FCS had previously been inserted into SARS-CoV-1, the causative agent of SARS, complicating differentiation of how such a feature may have appeared.

Closest Known Relatives of SARS-CoV-2, as of August

As of August, the closest known whole genome match to SARS-CoV-2—around **96 percent** identical—is **RaTG13**, a coronavirus collected from a bat in 2013 by the Wuhan Institute of Virology (WIV), according to academic literature. Scientific literature examining the genome of SARS-CoV-2 has identified at least some similarities to those of other naturally occurring coronaviruses in bats and pangolins, but an immediate precursor virus strain and animal reservoir have not been identified.

VIRUS NAME	PERCENT IDENTITY TO COVID-19 VIRUS	YEAR COLLECTED	LOCATION COLLECTED	ANIMAL COLLECTED
RaTG13	**96.2**	**2013**	**Yunnan Province, China**	**Bat**
RpYN06	94.5	2020	Yunnan Province, China	Bat
RmYN02	93.3	2019	Yunnan Province, China	Bat
RShSTT200	92.7	2010	Cambodia	Bat
RacCS203	91.5	2020	Thailand	Bat
PrC31	90.7	2018	Yunnan Province, China	Bat
Pangolin-CoV Guangdong	90.1	2019	Guangdong Province, China	Pangolin
ZC45	88.1	2015	Zhejiang Province, China	Bat
ZXC21	88.0	2015	Zhejiang Province, China	Bat
Guangxi pangolin-CoV	85.5	2017, 2018	Guangxi Zhuang Autonomous Region, China	Pangolin
Rc-o319	79.2	2013	Japan	Bat
RaTG15	77.6	2015	Yunnan Province, China	Bat

- The WIV previously created chimeras, or combinations, of SARS-like coronaviruses, but this information does not provide insight into whether SARS-CoV-2 was genetically engineered by the WIV.

No IC analysts assess that SARS-CoV-2 was the result of laboratory adaptation, although some analysts do not have enough information to make this determination. Repeated passage of a closely related virus through animals or cell culture—which we consider laboratory adaptation and not genetic engineering—could result in some features of SARS-CoV-2, according to publicly available information. However, it probably would take years of laboratory adaptation using the appropriate cell types and a virus that is more closely related to SARS-CoV-2 than ones currently known to generate the number of mutations separating SARS-CoV-2 from any known coronavirus strains, judging from scientific journal articles. Such processes would require differentiation and maintenance of primary cells and the development of appropriate animal models.

China's Lack of Foreknowledge of SARS-CoV-2

The IC assesses China's officials probably did not have foreknowledge that SARS-CoV-2 existed before WIV researchers isolated it after public recognition of the virus in the general population. Accordingly, if the pandemic originated from a laboratory-associated incident, they probably were unaware in the initial months that such an incident had occurred.

- Early in the pandemic, the WIV identified that a new virus was responsible for the outbreak in Wuhan. It is therefore assessed that WIV researchers pivoted to COVID-19-related work to address the outbreak and characterize the virus. These activities suggest that WIV personnel were unaware of the existence of SARS-CoV-2 until the outbreak was underway.

Two Plausible Hypotheses of Pandemic Origin

IC analysts assess that a natural origin and a laboratory-associated incident are both plausible hypotheses for how SARS-CoV-2 first infected humans. Analysts, however, disagree on which is more likely, or whether an assessment can be made at all, given the lack of diagnosticity of the available information. Most agencies are unable to make higher than low confidence assessments for these reasons, and confidence levels are tempered by plausible arguments for the opposing hypothesis. For these hypotheses, IC analysts consider an exposure that occurs during animal sampling activity that supports biological research to be a laboratory-associated incident and not natural contact. What follows is a look at the cases that can be made for these competing hypotheses.

The Case for the Natural Origin Hypothesis

Some IC analysts assess with low confidence that the first human COVID-19 infection most likely was caused by natural exposure to an animal that carried SARS-CoV-2 or a close progenitor virus—a virus that would likely be more than 99 percent similar to SARS-CoV-2. Four IC elements, the National Intelligence Council, and some analysts at elements that are unable to coalesce around either explanation are among this group. Analysts at these agencies give weight to China's officials' lack of foreknowledge and highlight the precedent of past novel infectious disease outbreaks having zoonotic origins, the wide diversity of animals that are susceptible to SARS-CoV-2 infection, and the range of scenarios—to include animal trafficking, farming, sale, and rescue—in China that enable zoonotic transmission. Although no confirmed animal source of SARS-CoV-2 has been identified, to include a reservoir or intermediate species, analysts that assess the pandemic was due to natural causes note that in many previous zoonotic outbreaks, the identification of animal sources has taken years, and in some cases, animal sources have not been identified.

- These analysts assess that WIV's activities in early 2020 related to SARS-CoV-2 are a strong indicator that the WIV lacked foreknowledge of the virus.

- They also see the potential that a laboratory worker inadvertently was infected while collecting unknown animal specimens to be less likely than an infection occurring through numerous hunters, farmers, merchants, and others who have frequent, natural contact with animals.

- Given China's poor public health infrastructure and the potential for asymptomatic infection, some analysts that lean towards a natural origin argue that China's infectious disease surveillance system would not have been able to detect the SARS-CoV-2 exposure as quickly as a suspected exposure in a laboratory setting.

History of Zoonotic Pathogen Emergence, Conditions in China Ripe for Zoonotic Spillover

Analysts that find the natural zoonotic spillover hypothesis the most likely explanation for the pandemic also note the wide diversity of animals that are susceptible to SARS-CoV-2 infection, range of scenarios—to include animal trafficking, farming, sale, and rescue—in China that would enable zoonotic

Comparing COVID-19 Pandemic to Past Select Viral Zoonotic Outbreaks

	Location of Emergence	Asymptomatic Infection Common	Reservoir Species and Year Identified	Probable Intermediate Species and Year Identified
COVID-19 *(2019–Present)*	China	Yes	Unknown	Unknown
Ebola *(2014–16)*	Guinea	No *(Probably)*	Bats *(Probably)*; N/A	Nonhuman primate *(Probably)*; N/A
MERS *(2012)*	Saudi Arabia, Jordan	Yes	Bats *(Probably)*; N/A	Dromedary camels; 2013
SARS *(2002–04)*	China	No *(Probably)*	Horseshoe bats; 2016	Masked palm civets and Raccoon dogs *(Possibly)*; 2003
Nipah *(1998–99)*	Malaysia	Yes	Fruit bats; 1999	Pigs; 1998
HIV-1[a] *(1970s–Present)*	Democratic Republic of Congo *(Probably)*	No *(Probably)*	Chimpanzees *(Probably)*; 1999	N/A

a. HIV is believed to have crossed from chimpanzees to humans in the 1920s; the first documented death occurred in the late 1960s.

transmission, and precedent of novel human infectious disease outbreaks originating from zoonotic transmission. Previous human coronavirus outbreaks, to include SARS-CoV-1 and Middle East Respiratory Syndrome coronavirus (MERS-CoV), occurred naturally and were linked to animal reservoirs with zoonotic transmission to humans, according to scientific literature.

- Extensive wildlife and livestock farming, wildlife trafficking, and live animal markets in China and historically lax government regulation—and even promotion—of these activities increase the probability that initial transmission occurred along one of these routes.

- Academic literature has revealed Wuhan markets sold live mammals and dozens of species—including raccoon dogs, masked palm civets, and a variety of other mammals, birds, and reptiles—often in poor conditions where viruses can jump among species, facilitating recombination events and the acquisition of novel mutations. SARS-CoV-2 can infect a range of mammals, including cats, dogs, pangolins, minks, raccoon dogs, and a variety of wild and domestic animals, according to academic literature.

- Wider Hubei Province has extensive farming and breeding of animals that are susceptible to SARS-CoV-2, including minks and raccoon dogs.

These analysts note that there is a precedent for viral vectors to travel long distances in China and cause infection elsewhere because of transportation and trade nodes, thereby widening and complicating the search for the specific zoonotic spillover incident. For instance, the bat coronavirus that is currently the closest known relative to the original SARS-CoV-1 was identified in Yunnan Province, even though the first SARS outbreak detected in humans occurred in Guangdong Province, hundreds of kilometers away.

The Case for the Laboratory-Associated Incident Hypothesis

One IC element assesses with moderate confidence that COVID-19 most likely resulted from a laboratory-associated incident involving WIV or other researchers—either through exposure to the virus during experiments or through sampling. Some analysts at elements that are unable to coalesce around either explanation also assess a laboratory origin with low confidence. These analysts place emphasis on academic articles authored by WIV employees indicating that WIV scientists conducted research on other coronaviruses under what these analysts consider to be inadequate biosafety conditions that could have led to opportunities for a laboratory-associated incident. These analysts also take into account SARS-CoV-2's genetic epidemiology and that the initial recorded COVID-19 clusters occurred only in Wuhan—and that WIV researchers who conducted sampling activity throughout China provided a node for the virus to enter the city.

WIV Research Includes Work With Animals That Carry Relatives of SARS-CoV-2

The analysts that find the laboratory-associated origin theory most likely assess that WIV researchers' inherently risky work with coronaviruses provided numerous opportunities for them to unwittingly become infected with SARS-CoV-2. Although the IC has no indications that WIV research involved SARS-CoV-2 or a close progenitor virus, these analysts note that it is plausible that researchers may have unwittingly exposed themselves to the virus without sequencing it during experiments or sampling activities, possibly resulting in asymptomatic or mild infection. Academic literature indicates that WIV researchers conducted research with bat coronaviruses or collected samples from species that are known to carry close relatives of SARS-CoV-2.

- Based on currently available information, the closest known relatives to SARS-CoV-2 in bats have been identified in Yunnan Province, and researchers bringing samples to laboratories provide a plausible link between these habitats and the city.
- These analysts also note that China's investigations into the pandemic's origin might not uncover evidence of a laboratory-associated incident if it involved only a small number of researchers who did not acknowledge or have knowledge of a potential infection.

> **WIV Illnesses in Fall 2019 Not Diagnostic**
>
> The IC assesses that information indicating that several WIV researchers reported symptoms consistent with COVID-19 in autumn 2019 is not diagnostic of the pandemic's origins. Even if confirmed, hospital admission alone would not be diagnostic of COVID-19 infection.

Biosafety Conditions for Specific Work Could Have Led to an Incident

The analysts that assess COVID-19 most likely originated from a laboratory-associated incident also place emphasis on information suggesting researchers in China used biosafety practices that increased the risk of exposure to viruses. Academic publications suggest that WIV researchers did not use adequate biosafety precautions at least some of the time, increasing the risk of a laboratory-associated incident.

The Role of the Huanan Seafood Wholesale Market

Some scientists and China's public health officials have shifted their view on the role of the Huanan Seafood Wholesale Market in the pandemic since early 2020. Some now view the market as a potential site of community spread rather than where the initial human infection may have occurred.

- On January 1, 2020, China's security authorities shut down the market after several workers fell ill in late December 2019. China focused early source tracing on the market and Hubei Province; association with the market was included as part of the early case definition.

- In January 2020, a scientific article that described clinical features of initial COVID-19 infections in China found that some COVID-19 patients did not have any known association with the market. Furthermore, there continues to be conflicting data with some academic articles and preprints noting that phylogenetic analysis of the available data on the earliest cases suggests that the progenitor virus may not have originated from the market.

China's Transparency Key to Determining COVID-19 Origin

The IC judges that closing persistent information gaps on the origins of COVID-19 is very likely to require greater transparency and collaboration from Beijing. The scientific community lacks technical data on a reservoir species, possible intermediate species, and closer relatives to SARS-CoV-2.

Data and Samples From Initial Cases: The global scientific community does not know exactly where, when, or how the first human infection with SARS-CoV-2 occurred. It lacks a complete picture of the initial cases in Wuhan—or potentially elsewhere in China—that would allow it to better understand potential sources of infection or conduct phylogenetic analysis that would help validate both hypotheses.

Information That Would Confirm Natural Outbreak: Searching for a natural reservoir or potential intermediate host requires collecting, isolating, and sequencing viruses from samples taken from potential host species and environments to search for viruses related to SARS-CoV-2, endeavors that require international collaboration, resources, and time.

- Information that the earliest confirmed COVID-19 cases were in individuals or families who spent time in rural regions or who were involved in animal trade or environments that facilitate close human-to-animal interactions could indicate that the virus was circulating within an animal reservoir and a zoonotic spillover event caused the first COVID-19 case in humans.

- However, some transmission pathways are fleeting, meaning an animal acquires a virus and evidence of infection vanishes, particularly if the animals are reared and harvested for agricultural or commercial purposes.

Information That Would Confirm Laboratory-Associated Incident: China's coronavirus research or related information from origins investigations by Beijing or international organizations could provide clear indications of a laboratory-associated incident or at least yield some new insights.

WIV's Publicly Available Coronavirus Research

IC analysts are examining published research from China for any indicators that would inform our understanding of COVID-19's origins. The WIV and other research groups in China published coronavirus articles in 2020 and 2021, including the discovery of the closest known relative of SARS-CoV-2, but at least some relevant data on coronaviruses of interest has either been unavailable or has not been published.

Although the WIV described the sampling trip to the mineshaft in Mojiang in Yunnan Province where it collected RaTG13 in 2016, it did not explicitly state that RaTG13 was collected from that mine until 2020. Similarly, the WIV collected eight other coronaviruses from the same mine in 2015 that it did not fully disclose until 2021. In some of these instances, however, the WIV has described unpublished work in webinars and interviews prior to publishing.

China Likely To Impede Investigation

The IC judges they will be unable to provide a more definitive explanation for the origin of COVID-19 unless new information allows them to determine the specific pathway for initial natural contact with an animal or to determine that a laboratory in Wuhan was handling SARS-CoV-2 or a close progenitor virus before COVID-19 emerged.

- For instance, Beijing limited the World Health Organization (WHO) investigation team's access to sites.
- In late July, China denounced a WHO plan for future investigations into COVID-19 origins, claiming that the proposal for future investigations was politicized. China's officials publicly rebuked the WHO's plans for a future study of labs in China, saying Beijing would not allow the WHO to engage in the "conspiracy theory."

China is also pushing its narrative that the virus originated outside China.

- Public statements from China's Government have continued to claim the virus originated from imported frozen food, an extremely unlikely theory.
- China's Government continues to spread allegations that the United States created or intentionally spread SARS-CoV-2 to divert attention away from Beijing.

Annex A: Definitions

Antibody: A protein produced during an immune response to a part of an infectious agent called an antigen.

Backbone: A genetic sequence used as a chassis upon which to build synthetic constructs, such as those used for cloning, protein expression, and production.

Biological weapon: A weapon that uses bacteria, viruses, toxins, fungi, and biochemical/biomolecule agents that can cause death or injury to humans, plants, or animals or destroy materials.

Biosafety: The application of knowledge, techniques, and equipment to prevent personal, laboratory, and environmental exposure to potentially infectious agents or biohazards. Four **Biosafety levels (BSL)** define the containment conditions under which biological agents can be safely manipulated. These standards range from moderate safety requirements for low-risk agents (BSL-1), to the most stringent controls for high-risk agents (BSL-4). China's standards range from P1–4.

Biosecurity: The protection, control of, and accountability for biological agents, toxins, and biological materials and information to prevent unauthorized possession, loss, theft, misuse, diversion, and accidental or intentional release.

Coronavirus: A common type of virus that can infect humans and/or animals. The human illness caused by most coronaviruses usually last a short time and presents symptoms consistent with the "common cold," such as a runny nose, sore throat, cough, and a fever.

COVID-19: An infectious disease caused by the **SARS-CoV-2** virus, which is a betacoronavirus.

Diagnostic information: Information that allows IC analysts to distinguish between hypotheses—in this case, the laboratory origin and natural origin theories.

DNA (deoxyribonucleic acid): A molecule that carries an organism's genetic blueprint for growth, development, function, and reproduction.

Epidemiology: The study of the distribution and determinants of health-related events in specified populations, and the application of this study to prevent and control health problems.

Furin cleavage site (FCS): A region in the spike protein of SARS-CoV-2 that enhances infection.

Gain-of-function: The IC considers this as a research method that involves manipulating an organism's genetic material to impart new biological functions that could enhance virulence or transmissibility (e.g., genetically modifying a virus to expand its host range, transmissibility, or severity of illness). The IC assesses that genetic engineering, genetic modification, and laboratory-adaptation can all be used for gain-of-function experiments, but are not inherently so. We address both genetic engineering and laboratory-adaptation in the body of this assessment; the IC is unaware of an agreed, international definition.

Genetically engineered or genetically modified viruses are intentionally altered, created, or edited using biotechnologies, such as Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR), DNA recombination, or reverse genetics. These viruses have intentional, targeted edits to the genome designed to achieve specific results, but unintentional genomic changes may also occur.

Genome: The genetic material of an organism. It consists of DNA (and sometimes RNA for viruses).

Genome sequencing: The process of determining the DNA or RNA sequence of an organism's genome, or its "genetic code." An organism's genetic code is the order in which the four nucleotide bases—adenine, cytosine, guanine, and thymine—are arranged to direct the sequence of the 20 different amino acids in the proteins that determine inherited traits.

Intermediate species/host: An organism that can be infected with a pathogen from a resevoir species and

passes the pathogen to another host species; infection is not sustained in this population.

Laboratory-adapted viruses have undergone natural, random mutations through human-enabled processes in a laboratory—such as repeated passage through animals or cells—that put pressure on the virus to more rapidly evolve. Specific changes to the viral genome are not necessarily anticipated in these processes, though the virus can be expected to gain certain characteristics, like the ability to infect a new species. This is a common technique used in public health research of viruses. We consider directed evolution to be under laboratory adaptation.

Laboratory-associated incidents include incidents that happen in biological research facilities or during research-related sampling activities.

Molecular biology: Study of the molecular basis of activities in and between cells. This includes techniques to amplify or join genetic sequences.

Naturally occurring viruses have not been altered in a laboratory. Viruses commonly undergo random mutations as part of the evolutionary process and can continue to change over time; mutations may enable a virus to adapt to its environment, such as evading host immune responses and promoting viral replication.

Outbreak: A sudden increase in occurrences of a disease in a particular time and place. Outbreaks include **epidemics**, which is a term that is reserved for infectious diseases that occur in a confined geographical area. **Pandemics** are near-global disease outbreaks.

Pangolin: An African and Asian mammal that has a body covered in overlapping scales. Pangolins are a natural reservoir of coronaviruses and researchers are investigating their potential role as an intermediate host for SARS-CoV-2.

Pathogen: A bacterium, virus, or other microorganism that can cause disease.

Phylogenetics: The study of the evolutionary relationships among groups of organisms.

Progenitor virus: A virus that is closely related enough—probably more than 99 percent—to SARS-CoV-2 to have been its direct ancestor or plausible immediate origin of the outbreak. The closest known relative to SARS-CoV-2 is only around 96 percent similar; to put this into context, humans and chimps are around 99 percent similar, demonstrating the signficant differences even at this similarity.

RaTG13: A coronavirus with the closest known whole genome to SARS-CoV-2, although it is widely believed to not be a direct ancestor of SARS-CoV-2.

Resevoir species/host: An organism that harbors a pathogen, which is endemic within the population.

RNA (ribonucleic acid): A molecule essential for gene coding, decoding, regulation, and expression. Certain viruses use RNA as a genetic blueprint.

Transmissibility: The measure of new infections initiated by an existing infection.

Virus: A replicating piece of genetic material—DNA or RNA—and associated proteins that use the cellular machinery of a living cell to reproduce.

Wet market: A market where fresh food and live and dead animals, including wildlife, are sold.

Zoonosis: An infection or a disease that is transmissible from animals to humans under natural conditions. A **zoonotic pathogen** may be viral, bacterial, or parasitic, and can sometimes be transmitted through insects, such as mosquitoes.

Zoonotic spillover: An initial infection or disease that is caused by contact between an animal and human under natural conditions.

Annex B: IC Examination of Open-Source Theories

IC analysts have examined a number of open-source articles from a variety of sources that have raised theories about SARS-CoV-2 and COVID-19's origin. The IC assesses that these theories generally do not provide diagnostic information on COVID-19 origins, and in some cases, are not supported by the information available to us. However, several have drawn on insightful methods or identified potential leads.

Theory of Abnormal Activity at the WIV in Fall 2019

The IC assesses that an assessment about abnormal activity at the WIV in fall 2019 lacks support and does not offer diagnostic insight. The Multi-Agency Collaboration Environment (MACE) published a report assessing that the pandemic began in October 2019 because of a release at the WIV.

- Although the methodology is insightful, the IC has concerns with the small data set and analytic rigor used to derive the group's findings, and our review of information directly contradicts some of its findings.

Theory That SARS-CoV-2 Was a Biological Weapon

The IC assesses that public claims from a Hong Kong virologist that Beijing created SARS-CoV-2 as a biological weapon are inconsistent with available technical information on coronaviruses. We assess that the articles contain several technical inaccuracies and omit key data points.

- Since September 2020, a virologist who worked in a WHO-affiliated laboratory in Hong Kong has publicly stated that Beijing created SARS-CoV-2 from bat coronaviruses and that China's researchers intentionally released it. The scientific community did not peer review these articles and some publicly rejected the articles' claims as scientifically unsound.

Theory That SARS-CoV-2 Was Genetically Engineered

The IC assesses that public claims that some distinguishing features in SARS-CoV-2 are the result of genetic engineering are not diagnostic of genetic engineering. The IC has been evaluating how SARS-CoV-2 could have developed these features and notes that the furin cleavage site (FCS)—a region in the spike protein that enables infection and has been the topic of open-source debate—can also be consistent with a natural origin of the virus.

We do not fully understand the diversity of natural coronaviruses or how often they recombine, suggesting that there are plausible natural means by which these features in SARS-CoV-2 could have emerged beyond what we currently understand.

- For example, the author of an article in April notes the SARS-CoV-2's FCS is unique among known betacoronaviruses. The author argues that such features are rare and so well-adapted for human infection that they are more likely emerged from laboratory work than from natural selection.

- Although an IC review of scientific literature has indicated that no known betacoronaviruses in the same subgenus have this FCS in the same region of the spike protein as SARS-CoV-2, similar FCSs are present in the same region of the spike protein as other naturally occurring coronaviruses, according to scientific articles.

We also do not find credible a now-withdrawn preprint article from two Indian educational institutes posted in January 2020 that asserted SARS-CoV-2 was genetically engineered using sequences from the human immunodeficiency virus. We assess it is unlikely that scientists would have chosen to intentionally engineer the specific sequences that were the focus of the scientific article.

Theory That SARS-CoV-2 Originated Outside China

We are aware of scientific studies claiming to have found SARS-CoV-2 viral fragments or antibodies in samples taken before November 2019 outside China. However, technical flaws in some of these studies, uncertainties in the methodologies, and in some cases, the lack of a credible review process make us skeptical of their utility in determining the pandemic's origin.

- We assess that the first cluster of confirmed COVID-19 cases arose in Wuhan, China, in late 2019, but we lack insight—and may never have it—on where the first SARS-CoV-2 infection occurred. Although all of the earliest confirmed cases of COVID-19 were documented in China's Hubei Province, where Wuhan is located, according to Western and China's press reports, it is plausible that a traveler came in contact with the virus elsewhere and then went to Wuhan.

- We continue to monitor scientific publications and discuss these issues with experts. Even if the virus is found to have existed outside China before the Wuhan outbreak, credible evidence of human infection would also be necessary to determine if the first COVID-19 outbreak began there.

Annex C: IC Approach to 90-Day Study

The NIC collaborated closely with the National Counterproliferation Center (NCPC), the National Intelligence Management Council (NIMC), IC agencies, and other USG entities and departments on this assessment. The IC kicked off the 90-day study by outlining the core intelligence questions that would be addressed over lines of effort—collection and analysis. These questions included:

- Did the outbreak begin through contact with infected domestic or wild animals or was it the result of a laboratory-associated incident?
- Was the virus genetically engineered?
- Is SARS-CoV-2 a biological weapon?

Collection: At the kick-off meeting for the 90-day study, the IC discussed core intelligence gaps to drive collection moving forward.

Analysis: The NIC had two separate structured analytic exercises to discuss both the underlying reporting and to strengthen argumentation moving into the drafting phase. Analysts at individual agencies also pursued various structured analytic techniques to build their own assessments.

- During a two-day-long in-person IC-wide **Analysis of Competing Hypothesis (ACH)** analytic exercise in June, analysts determined whether existing reporting was consistent or inconsistent with information in individual reports. This exercise allowed analysts to determine that most reporting was consistent with both hypotheses and the reporting that was inconsistent was deemed to be not credible.
- Before the start of drafting, the NIC hosted an IC-wide **Team A/Team B** analytic exercise to explore how the IC could strengthen either hypothesis through a debate style format. Agencies pulled from these conversations—along with the work conducted during and before the study—to solidify their consensus positions.

Annex D: Outside Review

The NIC conducted four rounds of outside review of the draft assessment. These sessions provided valuable feedback that we incorporated into the assessment. The NIC made some organizational changes in response to comments; comments included:

- Emphasize points of agreement.
- Provide additional definitions in the lexicon and ensure technical or intelligence jargon is explicitly explained.

Annex E: Questions

Answers to the following questions would help us better evaluate hypotheses related to the origins of COVID-19:

What additional information—to include timing, location, relevant animal exposures, occupational information, and clinical samples—is there on the earliest cases of COVID-19?

How were early cases investigated? What questions or tools were utilized for tracing contacts and contacts of those contacts?

What direct or indirect indicators of COVID-19 clusters is China aware of from early in the outbreak? This may include things like hospital occupancy rates or efforts to triage medical care outside of hospital facilities.

What insight can China provide on the search for the reservoir and potential intermediate species of the COVID-19 virus?

What insight can China provide on the search for the identification of a progenitor virus? Have any leading candidates or regions for spillover been identified?

What information, data, and/or samples does China have on wildlife or other animals present in the following markets in Wuhan:

- Huanan Seafood Wholesale Market
- Qiyimen Live Animal Market
- Baishazhou Market
- Dijiao Outdoor Pet Market

What information, data, and/or samples does China have on wildlife present in the other markets, wildlife rescue centers, and/or farms in Wuhan, across Hubei, in neighboring provinces, or in locations where live animals in Hubei Province are sourced from?